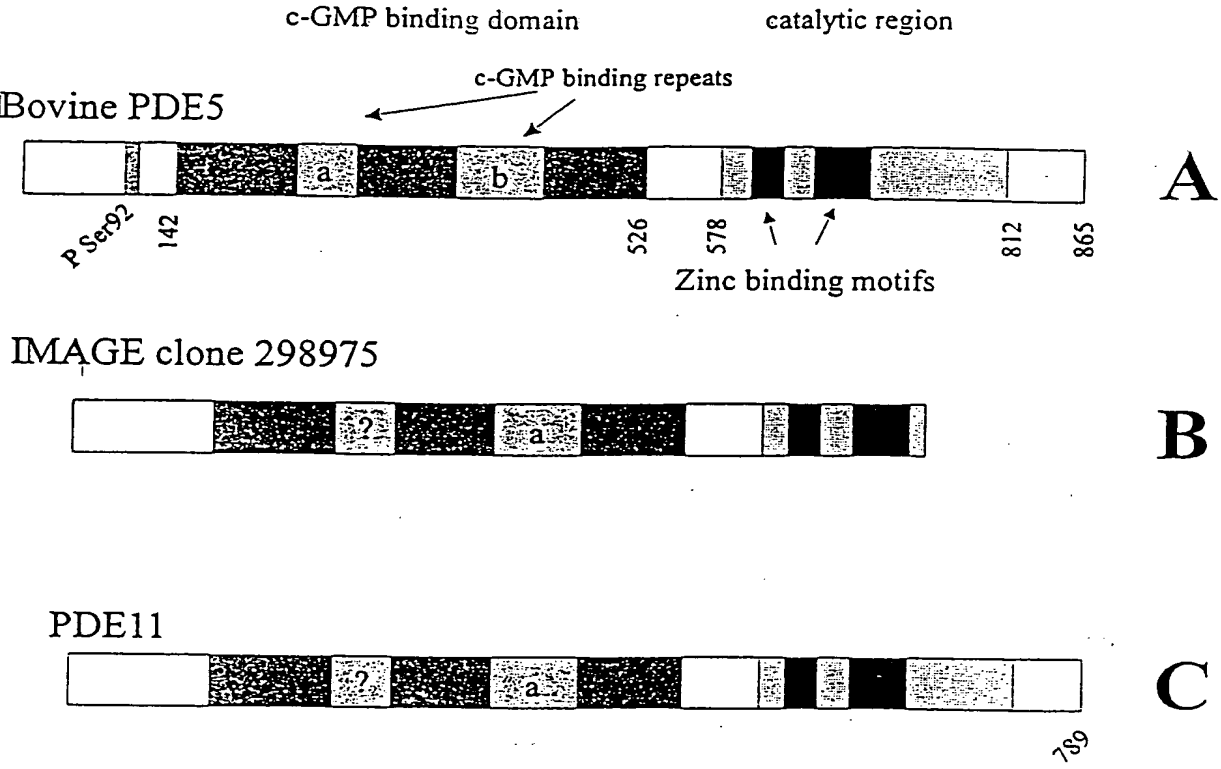


FIGURE 1

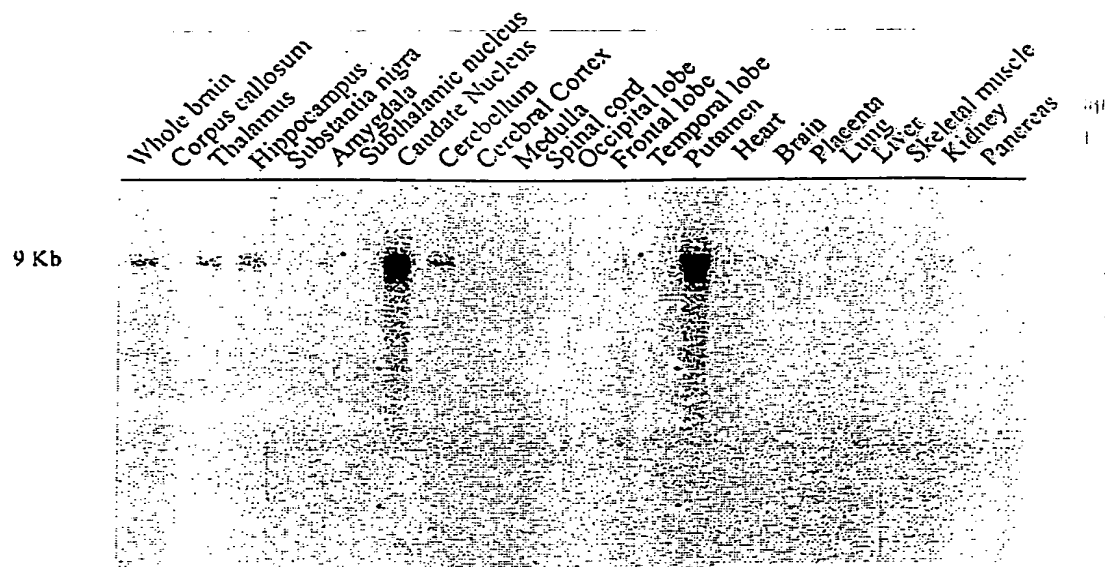
5



10

15

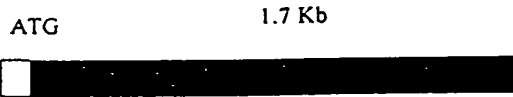
FIGURE 2



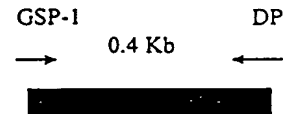
BEST AVAILABLE COPY

FIGURE 3

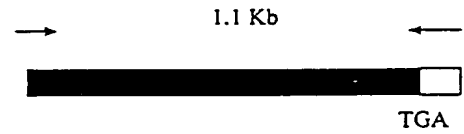
Original clone
IMAGE 298975



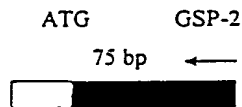
PCR on CN cDNA using a gene
specific primer (GSP) + a degenerate
primer (DP) designed from conserved
regions of PDE 5, 6



3' PCR product used as a probe
to isolate complete 3' sequence from
cDNA mini-library generated by
3' RACE



Splice variant isolated
by 5' RACE - Pde11a2



5

FIGURE 4

Figure 4A
SEQ ID No.1

```

TTCGGCTCCGACATGGAAGATGGACCTTCTAATAATGCGAGCTGCTTCCGAAGGCTGACC 60
GAGTGCTTCCTGAGCCCCAGTTTGACAGATGAAAAAGTGAAGGCATATCTTTCTCTTCAC 120
CCCCAGGTATTAGATGAATTTGTATCTGAAAGTGTTAGTGCGAGAGACAGTAGAGAAATGG 180
CTGAAGAGGAAGAACAACAATCAGAAGATGAATCAGCTCCTAAGGAAGTCAGCAGGTAC 240
CAAGATACGAATATGCAGGGAGTTGTATATGAACTAAACAGCTATATAGAACAACGGTTG 300
GACACAGGAGGAGACAACCAGCTACTCCTCTATGAACTGAGCAGCATCATTAAAATAGCC 360
ACAAAAGCCGATGGATTGCACTGTATTTCTTGGAGAGTGCAATAATAGCCTGTGTATA 420
TTCACGCCACCTGGGATAAAGGAAGGAAAAACCCCGCTCATCCCTGCTGGGCCCATCACT 480
CAGGGCACCACCGTCTCTGCTTATGTGGCCAAGTCCAGGAAAACACTGCTAGTAGAAGAC 540
ATCCTTGGAGATGAACGATTTCCAAGAGGTACTGGACTGGAATCAGGGACTCGTATCCAG 600
TCTGTTCTTTGCTTACCAATTGTCACTGCAATTGGTGACTTGATTGGTATTCTCGAGCTG 660
TATCGGCACCTGGGGCAAAGAAGCCTTCTGTCTTAGTCACCAGGAGGTTGCAACAGCAAT 720
CTTGCCCTGGGCTTCAGTAGCAATACATCAGGTGCAGGTATGCAGAGGCCTTGCCAAACAG 780
ACAGAATTGAATGACTTCTACTCGACGTATCAAAAAACATATTTTGATAACATAGTTGCA 840
ATAGATTCTCTACTTGAACACATAATGATATATGCAAAAAACCTGGTGAATGCCGATCGT 900
TGTGCACTTTTCCAGGTGGACCATAAGAACAAGGAGTTATATTCAGACCTTTTGTATATT 960
GGAGAGGAAAAGGAAGGAAAACCTGTCTTCAAGAAGACCAAGAGATAAGATTTTCAATT 1020
GAGAAAGGAATTGCTGGCCAAGTAGCAAGAACAGGGGAAGTCCTGAACATTCCAGATGCC 1080
TATGCAGACCCACGCTTTAACAGAGAAGTAGACTTGTACACAGGCTACACCACGCGGAAC 1140
ATCCTGTGCATGCCCATCGTCAGCCGAGGCAGCGTGATAGGTGTGGTGAGATGGTCAAC 1200
AAAATCAGTGGCAGTGCCTTCTCTAAAACAGATGAAAACAACTTCAAAATGTTTGCCGTC 1260
TTTTGTGCTTTAGCCTTACACTGTGCTAATATGTATCATAGAATTGCGCACTCAGAGTGG 1320
ATTTACCGGGTAACGATGGAAAAGCTGTCTCCTACCATAGCATTGTACTTCAGAAAGATGG 1380
CAAGGTCTCAATGCAATTCACCTTCCCGTGCCTCTGCAAAAGAAATTGAATTATTCAC 1440
TTTGACATTGGTCTTTTGA AAAACATGTGGCCTGGAATTTTTGTCTACATGGTTTCATCGG 1500
TCCTGTGGGACATCCTGCTTTGAGCTTGAAAAGTTGTGTGCTTTTATTATGTCTGTGAAG 1560
AAGAACTATCGGCGGGTTCTTTATCACAACCTGGAAGCATGCGGTCACTGTAGCACACTGC 1620
ATGTATGCCATACTTCAGAACAATCACACGCTTTTTCACAGACCTTGAGCGCAAAGGACTG 1680
CTGATTGCGTGTCTGTGTCTATGACCTGGACCACAGGGGCTTCAGTAACAGCTACCTGCAG 1740
AAGTTCGACCACCTCTGACCGCTCTCTACTCCACTTCCACCATGGAGCAGCACCCTTC 1800
TCCCAGACTGTGTCCATCCTTCAGTTGGAAGGGCACAATATCTTCTCCACTCTGAGCTCC 1860
AGTGAATATGAGCAGGTGCTTGAGATCATCCGCAAGCCATCATTGCCACAGACCTTGCT 1920
TTATACTTTGGAACAGGAAGCAGTTGGAAGAGATGTACCAGACCGGATCACTAAACCTT 1980
AATAATCAATCACATAGAGACCGTGTAATTGGTTTGATGATGACTGCCTGTGACCTTTGT 2040
TCTGTGACAAAACCGTGGCCCGTTACAAAATTGACGGCAAATGATATATATGCAGAATTC 2100
TGGGCTGAGGGTGATGAAATGAAGAAATTGGGAATACAGCCTATTCTATGATGGACAGA 2160
GACAAGAAGGATGAAGTCCCCCAAGGCCAGCTTGGGTTCTACAATGCCGTGGCCATTCCC 2220
TGCTATACAACCCCTTACCCAGATCCTCCCTCCCACGGAGCCTCTTCTGAAAGCATGCAGG 2280
GATAATCTCAGTCAGTGGGAGAAGGTGATTGAGGGGAGGAGACTGCAACCTGGATTTCA 2340
TCCCCATCCGTGGCTCAGAAGGCAGCTGCATCTGAAGATTGAGCACTGGTCACCCTGACA 2400
CGCTGTCCACCTACAGATCCTCATCTTGCTTCTTTGACATTCTTTTCTTTTGGGGG 2460
GGGTGGGGGGAACCTGCACCTGGTAACCTGGGGTGCAACCTCTTCAAGAAGGTAACATCA 2520
AATAAATAAGTCAAGCAGAAAAA 2557

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FIGURE 4 Continued

Figure 4B

SEQ ID No.2

MEDGPSNNASCFRRLTECFLSPSLTDEKVKAYLSLHPQVLDEFVSESVS AETVEKWLKRK 60
NNKSEDESAPKEVSRYQDTNMQGVVYELNSYIEQRLDTGGDNQLLLYELSSIIKIATKAD 120
GFALYFLGECNNSLCIFTPPGIKEGKPRLIPAGPITQGTTVSAYVAKSRKTLLVEDILGD 180
ERFPRGTGLESGETRIQSVLCLPIVTAIGDLIGILELYRHWGKEAFCLSHQEVATANLAWA 240
SVAIHQVQVCRGLAKQTELNDFLLDVSKTYFDNIVAIDSLLHEHIMIYAKNLVNADRCALF 300
QVDHKNKELYSDFDIGEEKEGKPVFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAYADP 360
RFNREVDLYTGYTTRNILCMPIVSRGSVIGVVQMVNKGSGSAFSKTDENNFKMFAVFCAL 420
ALHCANMYHRIRHSECIYRVTMKLSYHSICTSEEWQGLMQFTLPVRLCKEIELFHFHDIG 480
PFENMWPGIFVYVMVHRSCGTSCFELEKLCRFIMSVKKNYRRVPYHNWKHAVTVAHCMYAI 540
LQNNHTLFTDLERKGLLIACLCHDLDRGFSNSYLQKFDHPLTALYSTSTMEQHHFSQTV 600
SILQLEGHNIFSTLSSSEYEQVLEIIRKAI IATDLALYFGNRKQLEEMYQTGSLNLNQNS 660
HRDRVIGLMMTACDLCSVTKPWPVTKLTANDIYAEFWAEGDEMKKLGIQPIPMMDRDKKD 720
EVPQGQLGFYNAVAIPCYTTLTQILPPTPELLKACRDNLSQWEKVIRGEETATWISSPSV 780
AQKAAASED 789

FIGURE 5

Figure 5A
SEQ ID No.3

```

ACATAGCTGGGTGCAATGTAAGTGCCTGGCTGAAGTTTGACACGCGAACGGACGGCCCGC 60
TGGAAATTCTGTGCTATGAGCCGGAGTAGAAAGAGAGATTTGGACTCTGCAACACCAAGGT 120
AGTCGTTGAAGCCACAGTCGTGAATGGAGACCAGGAGTGAATAGTGGGAGTGAGCAGAAG 180
TCGGAGGATAGGACAGAAGAAGGCAGAGCCATGGAGCACCCCTGGAGAGGTGTGACCCGGC 240
AAGATCCTGAGATGGAAGGTAGCACGGCCTGGAGTTCAGAAGCGGAGCCTCAAGAGGGAA 300
GAAGCCAGATGCTCCAGAGAGCAGGTTTGACAGATGAAAAAGTGAAGGCATATCTTTCTC 360
TTCACCCCCAGGTATTAGATGAATTTGTATCTGAAAGTGTAGTGCAGAGACAGTAGAGA 420
AATGGCTGAAGAGGAAGAACAACAATCAGAAGATGAATCAGCTCCTAAGGAAGTCAGCA 480
GGTACCAAGATACGAATATGCAGGGAGTTGTATATGAACTAAACAGCTATATAGAACAAC 540
GGTTGGACACAGGAGGAGACAACCAGCTACTCCTCTATGAACTGAGCAGCATCATTAAAA 600
TAGCCACAAAAGCCGATGGATTGTCACTGTATTTCTTGGAGAGTGCAATAATAGCCTGT 660
GTATATTACGCCACCTGGGATAAAGGAAGGAAAACCCCGCTCATCCCTGCTGGGCCCA 720
TCACTCAGGGCACCACCGTCTCTGCTTATGTGGCCAAAGTCCAGGAAAACACTGCTAGTAG 780
AAGACATCCTTGGAGATGAACGATTTCCAAGAGGTACTGGACTGGAATCAGGGACTCGTA 840
TCCAGTCTGTCTTTGCTTACCAATTGTCACTGCAATTGGTGACTTGATTGGTATTCTCG 900
AGCTGTATCGGCCTGGGGCAAAGAAGCCTTCTGTCTTAGTCACCAGGAGGTTGCAACAG 960
CAAATCTTGCTGGGCTTCAGTAGCAATACATCAGGTGCAGGTATGCAGAGGCCTTGCCA 1020
AACAGACAGAATTGAATGACTTCCTACTCGACGTATCAAAAACATATTTTGATAACATAG 1080
TTGCAATAGATTCTCTACTTGAACACATAATGATATATGCAAAAAACCTGGTGAATGCCG 1140
ATCGTTGTGCACTTTTCCAGGTGGACCATAAGAACAAGGAGTTATATTAGACCTTTTTTG 1200
ATATTGGAGAGGAAAAGGAAGGAAAACCTGTCTTCAAGAAGACCAAAGAGATAAGATTTT 1260
CAATTGAGAAAGGAATTGCTGGCCAAGTAGCAAGAACAGGGGAAGTCTGAAACATTCCAG 1320
ATGCCTATGCAGACCCACGCTTTAACAGAGAAGTAGACTTGTACACAGGCTACACCACGC 1380
GGAACATCCTGTGCATGCCCATCGTCAGCCGAGGCAGCGTGATAGGTGTGGTGCAGATGG 1440
TCAACAAAATCAGTGGCAGTGCCCTTCTTAAACAGATGAAAAACAATTCAAAATGTTTG 1500
CCGTCTTTTGTGCTTTAGCCTTACACTGTGCTAATATGTATCATAGAATTCGCCACTCAG 1560
AGTGCAATTTACCGGGTAAAGATGGAAAAGCTGTCTTACCATAGCATTGTACTTCAGAAG 1620
AGTGGCAAGGTCTCATGCAATTCACCTTCCCGTGCCTCTGCAAAAGAAATTGAATTAT 1680
TCCACTTTGACATTTGGTCTTTTGAAAACATGTGGCCTGGAATTTTGTCTACATGGTTC 1740
ATCGGTCTGTGGGACATCCTGCTTTGAGCTTGAAGTTGTGTGCTTTTATTATGTCTG 1800
TGAAGAAGAACTATCGGCGGGTTCCTTATCACAACCTGGAAGCATGCGGTCACTGTAGCAC 1860
ACTGCATGTATGCCATACTTCAGAACAAATCACACGCTTTTTCACAGACCTTGAGCGCAAAG 1920
GACTGCTGATTGCGTGTCTGTGTCATGACCTGGACCACAGGGGCTTCAGTAACAGCTACC 1980
TGCAGAAGTTGACACACCTCTGACCGCTCTCTACTCCACTTCCACCATGGAGCAGCACC 2040
ACTTCTCCAGACTGTGTCCATCCTTCAGTTGGAAGGGCACAATATCTTCTCCACTCTGA 2100
GCTCCAGTGAATATGAGCAGGTGCTTGAGATCATCCGAAAGCCATCATTGCCACAGACC 2160
TTGCTTTATACTTTGGAAAACAGGAAGCAGTTGGAAGAGATGTACCAGACCGGATCACTAA 2220
ACCTTAATAATCAATCACATAGAGACCGTGTAATTGGTTTGATGATGACTGCCTGTGACC 2280
TTTGTTCTGTGACAAAACCGTGGCCCGTTACAAAATTGACGGCAAATGATATATATGCAG 2340
AATTCTGGGCTGAGGGTGATGAAATGAAGAAATTGGGAATACAGCCTATTCTATGATGG 2400
ACAGAGACAAGAAGGATGAAGTCCCCCAAGGCCAGCTTGGGTTCTACAATGCCGTGGCCA 2460
TTCCCTGCTATACAACCCTTACCCAGATCCTCCCTCCCACGGAGCCTCTTCTGAAAGCAT 2520
GCAGGGATAATCTCAGTCAGTGGGAGAAGGTGATTTCAGAGGGGAGGAGACTGCAACCTGGA 2580
TTTCATCCCCATCCGTGGCTCAGAAGGCAGCTGCATCTGAAGATTGAGCACTGGTCACCC 2640
TGACACGCTGTCCACCTACAGATCCTCATCTTGCTTCTTTGACATTCTTTTCTTTTTT 2700
GGGGGGGGTGGGGGGAACCTGCACCTGGTAACTGGGGTGCAAACCTCTTCAAGAAGGTAA 2760
CATCAAATAAATAAGTCAAGCAGAAAAAAAAAAAAAAAAA 2799

```

FIGURE 5 Continued

Figure 5B

SEQ ID No.4

MEGSTAWSSEAE PQEGRSQMLQRAGLTDEKVKAYLSLHPQVLDEFVSES VSAETVEKW LK 60
RKNNKSEDESAPKEVSRYQDTNMQGVVYELNSYIEQRLDTGGDNQ LLLYELSSIIKIATK 120
ADGFALYFLGECNNSLCIFT PPGIKEGK PRLIPAGPITQGT TVSAYVAKSRKTLLVEDIL 180
GDERFPRGTGLES GTRIQSVLCLPIVTAIGDLIGILELYRHWGKEAFCLSHQE VATANLA 240
WASVAIHQVQVCRGLAKQTE LNDFLLDVSKTYFDNIVAIDS LLEHIM IYAKNLVNADRCA 300
LFQVDHKNKELYS DLFDIGEEKEGKPVFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAYA 360
DPRFNREVDLYTGYTTRN ILCMPIVSRG SVIGVVQMVNKISGS AFSKTDENNFKMFAVFC 420
ALALHCANMYHRIRHSECIYRV TM EKLSYHSICTSEEWQGLMQFTLPVRLCKEIELFHFD 480
IGPFENMWPGIFVY MVHRSCGTSCFELEKLCRFIMSVKKNYRRVPYHNWKHAVTVAHCMY 540
AILQNNHTLFTDLERKGLLIAC LCHDL DHRGFSNSYLQKFDHPLTALYSTSTMEQH HFSQ 600
TVSILQLEGHNIFSTLS SSEYEQVLEIIRKAI IATDLALYFGNRKQLEEMYQTGSLNLNN 660
QSHRDRVIGLMMTACDLC SVTKPW PVTKL TANDIYA EFWAEGDEM KKLGIQPIPMMDRDK 720
KDEV PQGQLGFYNAVAIPCYTTLTQILP PTEPLLKACRDNLSQWEKVIRGEETATWISSP 780
SVAQKAAASED 791

FIGURE 5 Continued

Figure 5C

PDE11A1

MEDGPSNNASCFRRLTECFSLTDEKVKAYLSLHPQVLDEFVSESVAETVEKWLKRKNNKSEDESAPKEV

|

+++++

PDE11A2

MEGSTAWSSEAEPQEGRSQMLQRAGLTDEKVKAYLSLHPQVLDEFVSESVAETVEKWLKRKNNKSEDESAPKEV

FIGURE 6

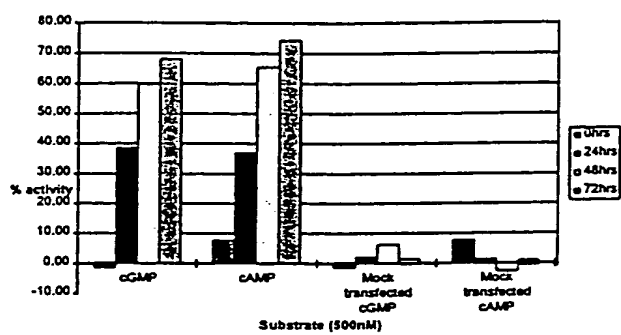
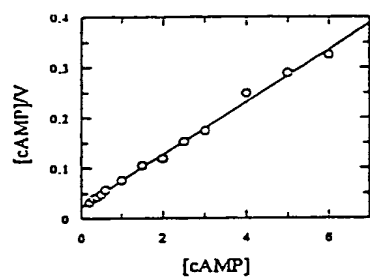


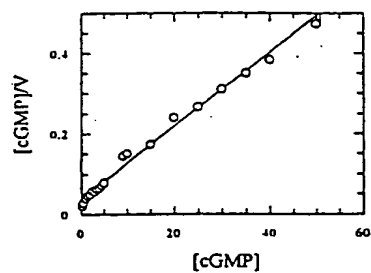
FIGURE 7

7A



Variable	Value	Std. Err.
Intercept	0.0238	0.0029 (Km/Vmax)
Slope	0.0521	0.0011 (1/Vmax)
Km	0.456	

7B



Variable	Value	Std. Err.
Intercept	0.0360	0.0038 (Km/Vmax)
Slope	0.0090	0.0002 (1/Vmax)
Km	4.0	

FIGURE 8

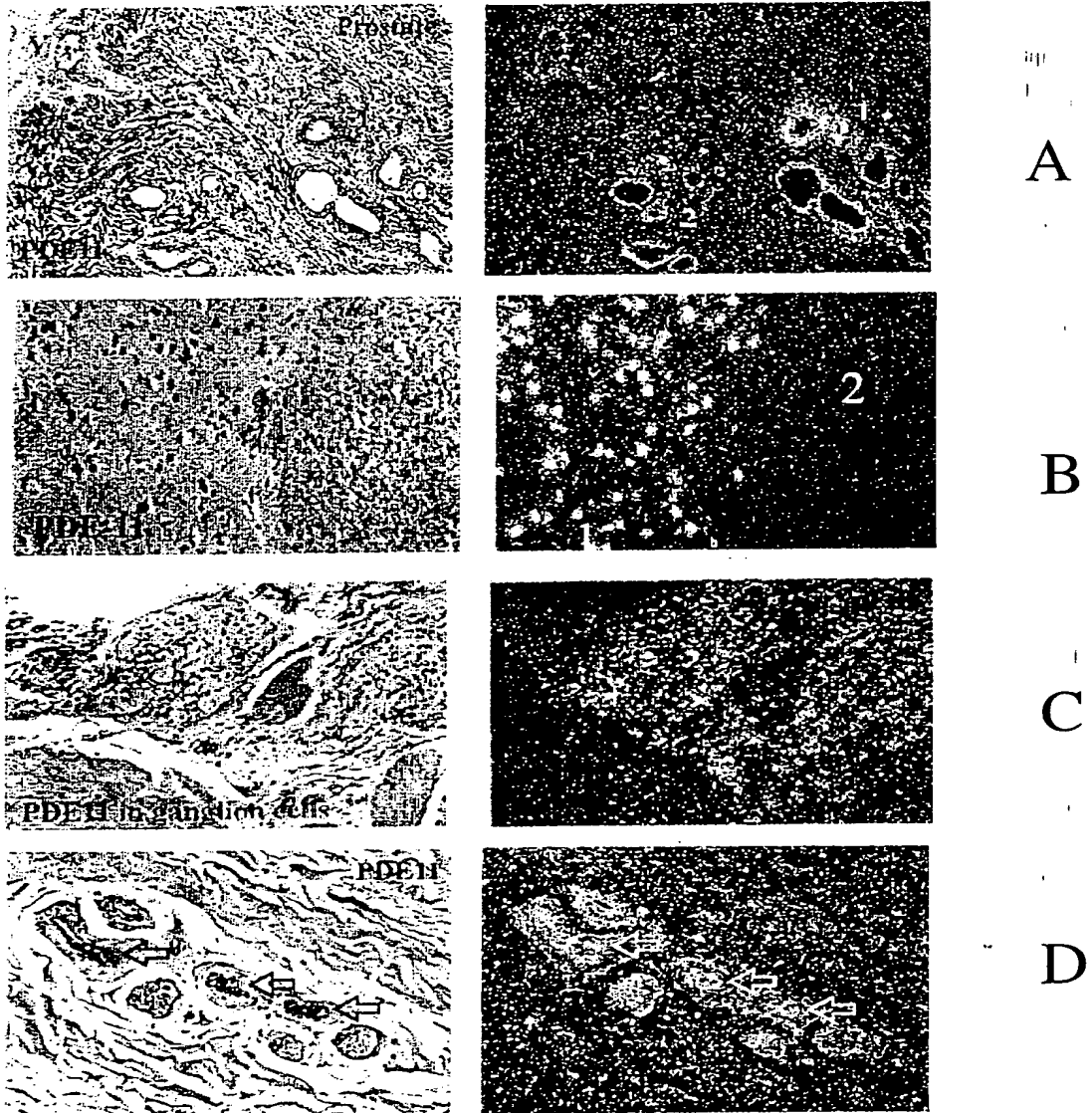


FIGURE 9

5

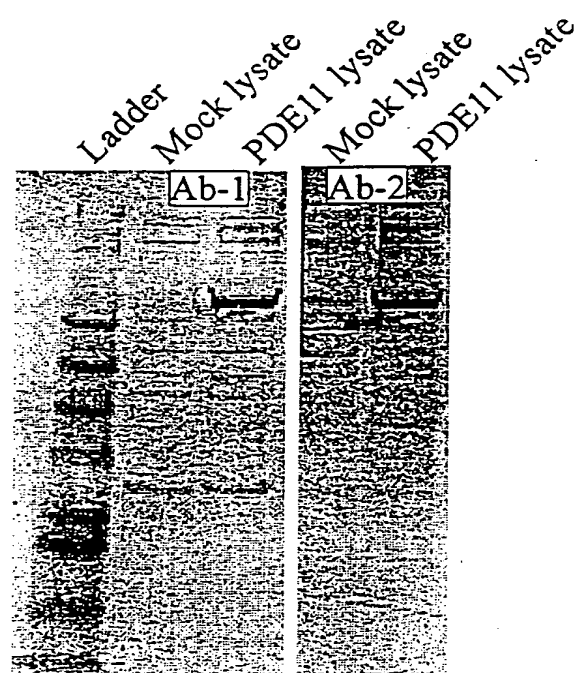


Figure 10

Length = 789

Score = 1527 (709.8 bits), Expect = 1.7e-213, P = 1.7e-213

Identities = 292/300 (97%), Positives = 298/300 (99%)

```
Query:   1 FLGECNNSLCVFIPPGMKEGQPRLIPAGPITQGTISAYVAKSRKTLLEDILGDERFPR 60
          FLGECNNSLC+F PPG+KEG+PRLIPAGPITQGT+SAYVAKSRKTLLEDILGDERFPR
Sbjct:  126 FLGECNNSLCIFTPPGIKEGKPRIPAGPITQGTTSAYVAKSRKTLLEDILGDERFPR 185

Query:   61 GTGLESGETRIQSVLCLPIVTAIGDLIGILELYRHWKEAFCLSHQEVATANLAWASVAIH 120
          GTGLESGETRIQSVLCLPIVTAIGDLIGILELYRHW KEAFCLSHQEVATANLAWASVAIH
Sbjct:  186 GTGLESGETRIQSVLCLPIVTAIGDLIGILELYRHWGKEAFCLSHQEVATANLAWASVAIH 245

Query:   121 QVQVCRGLAKQTELNDFLLDVSKTYFDNIVAIDSLEHIIYAKNLVNADRCALFQVDHK 180
          QVQVCRGLAKQTELNDFLLDVSKTYFDNIVAIDSLEHI+IYAKNLVNADRCALFQVDHK
Sbjct:  246 QVQVCRGLAKQTELNDFLLDVSKTYFDNIVAIDSLEHIMIYAKNLVNADRCALFQVDHK 305

Query:   181 NKELYSOLFDIGEEKEGKPIFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNRE 240
          NKELYSOLFDIGEEKEGKPFKKKTKEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNRE
Sbjct:  306 NKELYSOLFDIGEEKEGKPVFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNRE 365

Query:   241 VDLYTGYTTRNILCMPIVSRGSVIGVVQMVNKGSGSAFSKTDENNFKMFAVFCALALHCA 300
          VDLYTGYTTRNILCMPIVSRGSVIGVVQMVNKGSGSAFSKTDENNFKMFAVFCALALHCA
Sbjct:  366 VDLYTGYTTRNILCMPIVSRGSVIGVVQMVNKGSGSAFSKTDENNFKMFAVFCALALHCA 425
```

FIGURE 11

HumanPDE11A1_	ME--DGPSNNASCFRRLTECFLSPSLTDEKVKAYLSLHPQVLDEFVSESVAETVEKWLK
HumanPDE11A2_	ME--DGPSNNASCFRRLTECFLSPSLTDEKVKAYLSLHPQVLDEFVSESVAETVEKWLK
MousePDE11A3_	ME--DGPSNNASCFRRLTECFLSPSLTDEKVKAYLSLHPQVLDEFVSESVAETVEKWLK
HumanPDE11A1_	RKNNKSEDESAPKEVSRYQDTNMQGVVYELNSYIEQRLDTGGDNQLLLYELSSIIKIATK
HumanPDE11A2_	RKNNKSEDESAPKEVSRYQDTNMQGVVYELNSYIEQRLDTGGDNQLLLYELSSIIKIATK
MousePDE11A3_	RKNNKSEDESAPKEVSRYQDTNMQGVVYELNSYIEQRLDTGGDNQLLLYELSSIIKIATK
HumanPDE11A1_	ADGFALYFLGECNNSLCIFTPPGIKEGKPRIPAGPITQGTTVSAYVAKSRKTLLEDIL
HumanPDE11A2_	ADGFALYFLGECNNSLCIFTPPGIKEGKPRIPAGPITQGTTVSAYVAKSRKTLLEDIL
MousePDE11A3_	ADGFALYFLGECNNSLCIFTPPGIKEGKPRIPAGPITQGTTVSAYVAKSRKTLLEDIL
HumanPDE11A1_	GDERFPRGTGLESRTIQSVLCLPIVTAIGDLIGILELYRHWGKEAFCLSHQEVATANLA
HumanPDE11A2_	GDERFPRGTGLESRTIQSVLCLPIVTAIGDLIGILELYRHWGKEAFCLSHQEVATANLA
MousePDE11A3_	GDERFPRGTGLESRTIQSVLCLPIVTAIGDLIGILELYRHWGKEAFCLSHQEVATANLA
HumanPDE11A1_	WASVAIHQVQVCRGLAKQTELDNDFLLDVSKTYFDNIVAIDSLEHIMIYAKNLVNADRC
HumanPDE11A2_	WASVAIHQVQVCRGLAKQTELDNDFLLDVSKTYFDNIVAIDSLEHIMIYAKNLVNADRC
MousePDE11A3_	WASVAIHQVQVCRGLAKQTELDNDFLLDVSKTYFDNIVAIDSLEHIMIYAKNLVNADRC
HumanPDE11A1_	LFQVDHKNKELYSDLFDIGEEKEGKPVFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYA
HumanPDE11A2_	LFQVDHKNKELYSDLFDIGEEKEGKPVFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYA
MousePDE11A3_	LFQVDHKNKELYSDLFDIGEEKEGKPVFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYA
HumanPDE11A1_	DPRFNREVDLYTGYTTRNLCMPIVSRGSGVIGVQMVNKGSGSAFSTDENNFQMAFVFC
HumanPDE11A2_	DPRFNREVDLYTGYTTRNLCMPIVSRGSGVIGVQMVNKGSGSAFSTDENNFQMAFVFC
MousePDE11A3_	DPRFNREVDLYTGYTTRNLCMPIVSRGSGVIGVQMVNKGSGSAFSTDENNFQMAFVFC
HumanPDE11A1_	ALALHCANMYHRIRHSECIYRVTEKLSYHSICTSEEWQGLMQFTLPVRLCKEIELFHFD
HumanPDE11A2_	ALALHCANMYHRIRHSECIYRVTEKLSYHSICTSEEWQGLMQFTLPVRLCKEIELFHFD
MousePDE11A3_	ALALHCANMYHRIRHSECIYRVTEKLSYHSICTSEEWQGLMQFTLPVRLCKEIELFHFD
HumanPDE11A1_	IGPFENMWPGIFVYMHVRS CGTSCFELEKLCRFIMSVKQNYRRVPYHNWKHAVTVAHCMY
HumanPDE11A2_	IGPFENMWPGIFVYMHVRS CGTSCFELEKLCRFIMSVKQNYRRVPYHNWKHAVTVAHCMY
MousePDE11A3_	IGPFENMWPGIFVYMHVRS CGTSCFELEKLCRFIMSVKQNYRRVPYHNWKHAVTVAHCMY
HumanPDE11A1_	AILQNNHTLFTDLERKGLLIACLDHLDHGRGFSNSYLQKFDHPLTALYSTSTMEQHHSQ
HumanPDE11A2_	AILQNNHTLFTDLERKGLLIACLDHLDHGRGFSNSYLQKFDHPLTALYSTSTMEQHHSQ
MousePDE11A3_	AILQNNHTLFTDLERKGLLIACLDHLDHGRGFSNSYLQKFDHPLAALYSTSTMEQHHSQ
HumanPDE11A1_	TVSILQLEGHNIFSTLSSSEYEQVLEIIRKAIATDLALYFGNRKQLEEMYQTGSLNLNN
HumanPDE11A2_	TVSILQLEGHNIFSTLSSSEYEQVLEIIRKAIATDLALYFGNRKQLEEMYQTGSLNLNN
MousePDE11A3_	TVSILQLEGHNIFSTLSSSEYEQVLEIIRKAIATDLALYFGNRKQLEEMYQTGSLNLNN
HumanPDE11A1_	QSHRDRVIGLMMTACDLCSVTKPWPVTKLTDANDIYAEFWAEGDEMCKLGIQPIPMMDRDK
HumanPDE11A2_	QSHRDRVIGLMMTACDLCSVTKPWPVTKLTDANDIYAEFWAEGDEMCKLGIQPIPMMDRDK
MousePDE11A3_	QSHRDRVIGLMMTACDLCSVTKLWPVTKLTDANDIYAEFWAEGDEMCKLGIQPIPMMDRDK
HumanPDE11A1_	KDEVPOGQLGFYNAVAIPCYTTTLTQILPPTPEPLKACRDNLSQWEKVIRGEETATWISSP
HumanPDE11A2_	KDEVPOGQLGFYNAVAIPCYTTTLTQILPPTPEPLKACRDNLSQWEKVIRGEETATWISSP
MousePDE11A3_	RDEVPOGQLGFYNAVAIPCYTTTLTQILPPTPEPLKACRDNLSQWEKVIRGEETATWISSP
HumanPDE11A1_	SVAQKAAASED-----
HumanPDE11A2_	SVAQKAAASED-----
MousePDE11A3_	GPAPSKSTPEKLNKVED